

This paper investigates the precise mechanisms driving the cessation of transmission in classical epidemic models, specifically the SIR model. Introduction Understanding the mechanisms behind the cessation of infectious disease outbreaks is a core question of modern epidemiology. Methodology We employed both an ODE-based deterministic SIR model and a stochastic SIR simulation on an Erdős-Rényi network. Analytical Model (ODE) We solved the standard SIR equations[0]:
$$\frac{dS}{dt} = -\beta \frac{SI}{N}, \quad \frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I, \quad \frac{dR}{dt} = \gamma I$$
 Simulation used scipy.integrate.odeint. Network-based SIR Simulation A stochastic, network-aware SIR simulation was constructed using FastGEMF over a random network. Results Figure (ODE/analytical) and Figure (network simulation) display the time courses of S, I, and R populations under the deterministic and stochastic models, respectively. [h] [width=0.6]figure-ODE.png Trajectories of susceptible (S), infected (I), and removed (R) compartments under the deterministic model. [h] [width=0.6]figure-network.png Trajectories of S, I, and R populations from network-aware SIR simulation.

	Model	S_{final}	I_{final}	R_{final}	Extinction mode
[ht] Summary of Final Outcomes and Transmission Extinction Mode	ODE (Analytic)	1075.2	0.09	8924.7	Infectives extinct
	Network	0.0	0.0	10000.0	Both infectives and susceptibles extinct

Discussion Our results show a clear distinction in the mechanism of chain breakage. The classical (ODE) SIR model predicts that the infection chain ceases due to the depletion of susceptibles. Conversely, the network-based stochastic simulation resulted in near-total exhaustion of susceptibles, with all individuals eventually becoming removed. These nuances are critical when interpreting epidemiological data and when using SIR-type models for forecasting or intervention strategies. Conclusion The breakage of the transmission chain in SIR epidemics can occur due to the extinction of infectives or by the exhaustion of susceptibles, depending on the model and network structure.

*References

99

Compartmental models (epidemiology). Wikipedia. [https://en.wikipedia.org/wiki/Compartmental_models\(epidemiology\)](https://en.wikipedia.org/wiki/Compartmental_models(epidemiology)). Accessed 2023-10-27.
P. Berenbrink et al., "On Early Extinction and the Effect of Travelling in the SIR Model", Proceedings of Machine Learning Research, vol. 130, pp. 1040–1050, 2020.

Code and Reproducibility Full Python scripts for analytic (ODE) and GEMF-based network SIR simulation are available at https://github.com/berenbrink/sir_models.
output/sir_analytical_ode_sim.py
output/sir_network_sim.py
output/analyze_extinction_sequence.py
output/plot_analysis_no_sns.py